

AMENDMENT TO THE SPECIFICATION

Please replace the last paragraph on page 14, numbered as paragraph [0050] with the following replacement paragraph:

[0050] BLASTN was performed for each one of the twelve clusters against the genomic sequences from *Populus trichocarpa* made available by the Joint Genome Institute, US Department of Energy as part of the "Populus Genome Sequencing Project" (genome.jgi-psf.org/poplar0/poplar0.info.html). Selected nucleotide regions from each cluster corresponding to putative exons were used as driver sequences in the retrieval of genomic sequence reads comprising the transcription initiation region and adjacent upstream promoter sequences. These genomic reads were assembled using the PHRAP (Gordon et al. (1998) *Genome Res.* 8:195-202) program to obtain a contig encompassing approximately 700 to 3500 nucleotides of putative promoter region upstream from the transcription initiation point (+1 nucleotide, which corresponds to the beginning of the respective mRNA). These contigs contain the promoter regions for each of the genes encoding the mRNAs represented by the twelve clusters concluded to be preferably expressed in the cambium and/or in the xylem tissues of *Populus*. These twelve promoter regions correspond to sequences disclosed herein under SEQ ID NOS.: 1-12.